

GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 15, 2003, 23:25:27 ; Search time 103.105 Seconds
(without alignments)
2525.515 Million cell updates/sec

Title: US-08-978-217-16

Perfect score: 1985

Sequence: 1 MATCEISNVFSNYFNAMYS.....YKFKNNSGCKEKEVGESRN 371

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 501302 segs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712	86.2	1915	10	US-09-964-824A-101
2	1712	86.2	1915	10	US-09-964-824A-563
3	1712	86.2	1915	10	US-09-880-107-3420
4	1712	86.2	1915	10	US-09-967-768A-192

5	1712	86.2	1917	9	US-10-025-380-1105	Sequence 1105, Ap
6	1712	86.2	1917	10	US-09-922-217-1105	Sequence 1105, Ap
7	1712	86.2	1996	10	US-09-925-301-207	Sequence 207, App
8	928.5	46.8	626	9	US-10-025-380-853	Sequence 853, App
9	928.5	46.8	626	10	US-09-922-217-853	Sequence 853, App
10	928.5	46.8	626	10	US-09-813-263-853	Sequence 853, App
11	833.5	42.0	563	9	US-10-025-380-944	Sequence 944, App
12	833.5	42.0	563	10	US-09-922-217-944	Sequence 944, App
13	833.5	42.0	563	10	US-09-833-263-944	Sequence 944, App
14	803	40.5	502	10	US-10-076-622-282	Sequence 282, App
15	803	40.5	502	10	US-09-604-287A-282	Sequence 282, App
16	803	40.5	502	12	US-10-007-805-282	Sequence 282, App
17	803	40.5	502	10	US-09-998-598-2290	Sequence 2290, App
18	765	38.7	1426	10	US-09-925-297-309	Sequence 309, App
19	590.5	29.5	1429	10	US-09-764-864-320	Sequence 320, App
20	585	28.0	1437	10	US-09-998-598-2216	Sequence 2216, App
21	555.5	28.0	852	9	US-09-232-880-44	Sequence 44, App1
22	543	27.4	852	9	US-10-012-896-44	Sequence 44, App1
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29	543	27.4	852	10	US-09-115-453-44	Sequence 44, App1
30	527.5	26.6	355	10	US-09-867-701-4818	Sequence 4818, App
31	527.5	26.6	5045	9	US-09-974-298-12	Sequence 12, App1
32	442	22.3	440	10	US-09-960-352-11873	Sequence 11873, A
33	435	21.9	441	10	US-09-998-598-32	Sequence 32, App1
34	363	18.3	451	10	US-09-864-761-14745	Sequence 14745, A
35	290	14.6	593	10	US-09-864-761-31274	Sequence 31274, A
36	285	14.4	196	10	US-09-998-598-1740	Sequence 1740, Ap
37	253	12.7	174	10	US-10-098-841-44	Sequence 44, App1
38	235.5	11.9	3653	9	US-10-098-841-45	Sequence 45, App1
39	235	11.8	3591	9	US-09-902-772-3	Sequence 3, App11
40	234.5	11.8	1894	10	US-09-126-945B-1	Sequence 1, App11
41	233.5	11.8	1905	10	US-09-866-358-2	Sequence 2, App11
42	233.5	11.8	4190	10	US-09-962-833-111	Sequence 11, App
43	228	11.3	1447	9	US-09-902-772-1	Sequence 1, App11
44	225	11.2	507	9	US-10-015-219-489	Sequence 489, App

ALIGNMENTS

RESULT 1
US-09-964-824A-101
; Sequence 101, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964, 824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236, 033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-101

Alignment Scores: 2.42e-172 Length: 1915
Pred. No.: 1712.00 Matches: 323
Score:

Percent Similarity: 92.74% Conservative: 22
 Best Local Similarity: 86.83% Mismatches: 25
 Query Match: 86.25% Indels: 2
 DB: 10 Gaps: 2

US-08-978-217-16 (1-371) x US-09-964-824A-101 (1-1915)

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Qy 1 MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
Db 120 ATGGCTGCACTGTGAGATTAGCAACATTTTACCACTACTTCCAGTGCAGTATGACACG 179

Qy 21 SerGluAapProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db 180 TCGAGAGACTCCACCCCTGCTCTCTCCCTGCTGCCACCTTGGGGCCCATGACTTG 239

Qy 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluLysAlaSerTrpThr 59
Db 240 GTACTGACCCCTGAGAACCCCGACATGTCATTGAGGGTACAGAGAAGGCCAGCTGGTG 299

Qy 60 SerGluAapProGlnPheTrpSerTrpThrGlnValLeuGluTrpIleSerTyrGlnVal 79
Db 300 GGGGAAACGCCCACTTCTGTGCGAAGACGACGTTCTGCACTGGATCAGTACCAAGTG 359

Qy 80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99
Db 360 GAGAAAGAACAGTACGACGCAAGCCCACTTGACTTCCAGATGTGACATGATGAGCGCC 419

Qy 100 ThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119
Db 420 ACCCTCTGCATTTGTCCTTAGAGAGCTGCGTCTGTGTTGGCTCTGCGGAGCAACA 479

Qy 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle 139
Db 480 CTCACATGCCACGCTCGAGACTCTCACTTCCACTCTTCTGAGAGACTCAGTTGGATCATT 539

Qy 140 GluLeuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGlyProPhe 159
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Qy 160 AspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyArgGlnAlaSerProTyr 179
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Qy 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
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Qy 220 AspLeuThrGluSerLysValPheProArgAspAspPheThrAspTyrLysIleGlu 239
Db 777 GATCCCATGTAGGAGAGCTCTTCCCAAGCATGCTTTCTGATGTGCAAGAGGGGGAT 836

Qy 240 ProLysHisGlyLysArgLysArgLysArgProArgLysLeuSerIleGluTyrTrpAsp 259
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Qy 260 CysLeuGluGlyLysLysSerLysHisAlaProArgLysThrHisLeuTrpIlePheIle 279
Db 897 TGCTCGAGGGGAGAGAGAGCAAGCAGCGGCCAGAGGACCACTGTGGGAGTTCAATC 956

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RESULT 2

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US-09-964-824A-563
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; FILE REFERENCE: 689290-73
; CURRENT FILING DATE: US/09/964, 824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236, 033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-563

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Alignment Scores:

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Pred. No.: 2,42e-172 Length: 1915
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
Gaps: 2

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US-08-978-217-16 (1-371) x US-09-964-824A-563 (1-1915)

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Qy 1 MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
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Qy 80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99
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Qy 100 ThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119
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Qy 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle 139
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; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-MO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3420
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843

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US-09-880-107-3420
Alignment Scores:
Pred. No.: 2,42e-172 Length: 1915
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: 10 Gaps: 2

US-08-978-217-16 (1-371) x US-09-880-107-3420 (1-1915)
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DB 120 ATGGCTGCAACCTGTGAGATTAGTAAATTTTAAAGAACTTCACTGAGTGAAGTACAGC 179
QY 21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
DB 180 TCGAGGACTCCACCCCTGGGCTCTGTTCCCTGCTGCCACCTTGGGGCCGAGACTTG 239
QY 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluLysAlaSerTrpThr 59
DB 240 GTACTGACCTTGAGCAACCCCGAGATGTATTGGAGGTTACAGAAAGCCAGCTGTTG 299
QY 60 SerGluArgProGlnPheTyrPserLysThrGlnValLeuGluLysLysTyrGlnVal 79
DB 300 GGGGAACAGCCCGAGTCTGTGGTGAAGACGAGGTTCTGAGCTGAGTCACTCAAGTG 359
QY 80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99
DB 360 GAGAAAGCAAGTACGACGGAACGCGCATTTGACTTCCAGATGTGACATGATGGGCGC 419
QY 100 ThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119
DB 420 ACCCTGCAATTGTGCTCTTGAAGAGCTGCTGCTCTTGGGCTCTGGGGACCA 479
QY 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIle 139
DB 480 CTCATCTCCAGCTGGAGAGCTCACTTCAGCTCTTCTGATGAGCTCAGTTGGATCAT 539
QY 140 GluLeuLeuGluYsaPglYMeTserPheGlnGluSerLeuGluYsaPleuGluYProPhe 159
DB 540 GAGCTGCTGAGAAAGATGAGCATGCTTCACAGAGCCCTTA---GACCAGAGGCCCTTT 596
QY 160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyr 179
DB 597 GACCAGGAGGCCCTTTCAGAGAGCTGTGACGACGCTGAGCAAGCCAGCCCTTAC 656
QY 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
DB 657 CACCCCGCAGCTGTGGCCGAGAGGCCCTCCCTGGCAGCTTGACGTCTCCACCGCA 716
QY 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
DB 717 GGGACTGTGCTTCTCGAGAGCTCCCACTCCAGACTCCCGTGAAGTGAAGTGAAGCTG 776
QY 220 AspLeuThrGluSerLeuValPheProArgAspAspPheThrAspTyrLysLysGlu 239
DB 777 GATCCCACTATGGCAAGCTTCTCCAGCGCATGTTTCTGTCAGTCCAGAAAGGGGAGAT 836
QY 240 ProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAsp 259
DB 837 CCCAAGACCGGAAAGCGGAAACGAGGCCGCGCCGAAAGCTGAGCAAAAGACTAGGGAGC 896
QY 260 CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrPgluPheIle 279
DB 897 TGCTCGAGGGCAAGAGAGCAAGCAGCGCCAGAGAGCCCACTGCTGGGAGTTTATC 956
QY 280 ArgAspIleLeuIleHisProGlnLeuLeuAsnGluLysLeuMetLysTrpGluAsnArgHis 299
DB 957 CGGACACTCTCATCCACCCGAGACTCAACAGAGGCTCTGAAAGTGGAGAAATCGGCAT 1016
QY 300 GluGlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTyrPgluLysLys 319

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Db 1017 GAAGCGCTTCTCAATTCTCTGCGCTCCAGGCTGTGGCCCAACTATGGGGCCAAAGAAA 1076

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Db 1077 AAGACAGAACATGACCTAGCAGAGAAGCTGAGCCGGGCCATGAGTACTACTACAAACGG 1136

Qy 340 GluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer 359

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RESULT 4

US-09-967-768A-192

Sequence 192: Application US/09967768A

Patent No. US20020150877A1

GENERAL INFORMATION:

APPLICANT: Augustus, Meena

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-72

CURRENT APPLICATION NUMBER: US/09/967,768A

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,034

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 325

SOFTWARE: PatentIn version 3.0

SEQ ID NO 192

LENGTH: 1915

TYPE: DNA

ORGANISM: Homo sapiens

US-09-967-768A-192

Alignment Scores:

Pred. No.: 2,42e-172 Length: 1915

Score: 1712.00 Matches: 323

Percent Similarity: 92.74% Conservative: 22

Best Local Similarity: 86.83% Mismatches: 25

Query Match: 86.25% Indels: 2

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Qy 1 MetAlaAlaThrCysGluLysSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20

Db 120 ATGGCTGCACCTGTGAGATTAGCAACATTTTACCAACTACTTCAAGTCCGATGACACG 179

Qy 21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39

Db 180 TCGGAGGACTCCACCTGGCCCTCTGTTCCCTGCTGCACCACTTTGGGGCCGATGACTTG 239

Qy 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluLysAlaSerTyrThr 59

Db 240 GATACGACCCCTGAGCAACCCCGAGATGTCATTGGAGGGTACAGAAAGGCCAGCTGGTGG 299

Qy 60 SerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTyrGlnTyrSerTyrGlnVal 79

Db 300 GGGGAAACACCCCAAGTTCTGCTCGAAGACGCAAGTTCGATGATGATGATGATGATGATG 359

Qy 80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99

Db 360 GAGAGAACCAAGTACAGACGCAAGCCGATGACTTCTCAGATGATGATGATGATGATGATG 419

Qy 100 ThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119

Db 420 ACCCTCTGCAATTGTGCCCTTGAAGAGCTGCGTCTGTGCTTTGGGCTCTGGGGAGACCA 479

Oy	120	LeuhtlaaqlneukrgrapsleuthreansemserSerAspGluLeuSertPrllele	139
Db	480	CTCCATGCCAGGTGGGAACCTTCACCTTCTTGATGACTCGTAGTGATCATTT	539
Oy	140	GluLeuLeuLgluYsaAspGlyMetSerPheIngInuSerLeuGlyAspLeuGlyProphe	159
Db	540	GAGCTGCTGGAGAAGATGGCATTGGCCTTCCAGAGAGGCCCTA---GACCAGGGCCCTTT	596
Oy	160	AspIngIyserProPheLaqngLuLeuLeuAapApGlyArgInalaserProtyr	179
Db	597	GACCAAGGCAGCCCCCTTTGCCAGAGAGCTGGACGACGGCTGACGAAGCCAGCCCCTAC	656
Oy	180	TyrCyseSerThrTyrgLyProGlyAlaProSerProGlySeraAPValSerThrala	199
Db	657	CACCCCGGACGCTGTGACGAGAGCCCTCTCCCTGGACACTTGACGTCCTCACCGCA	716
Oy	200	ArgThrAlathrProGlnInuSerHisAlaserAspSerGlyGlySeraAPValAspleu	219
Db	717	GGGACTGTCCTCTTCGGAGACTCCCACTCTCTACAGCTCCGGTGAATGACGTGGACTTG	776
Oy	220	AspleuThrGluSerLySaI PheProArghaPaPheThrRaPTyrvLyvLyGlyGlu	239
Db	777	GATCCCACTAGTGGCAAGCTCTTCCCAAGCGATGGTTTTCTGTACTCGACAAGAGGGGAT	836
Oy	240	ProlyHhaglYsaRgLYsaRgLYaRgProARgLYsaSerLyvGluTYTPAP	259
Db	837	CCCAAGGACGGGAAGCGGAAGCGAGCCGGCCCGAAAGCTGACCAAGATCTGGGAC	896
Oy	260	CysLeuGluGlyvLyvSeserLyshAlaProArgGlyThrhIsleuTrpGluPheIe	279
Db	897	TGTCTCGAGGGCAAGAAGAGCAACGCGGCCACAGACCCACCTGTGGAGTTTCATC	956
Oy	280	ArgAspIleLeuIlehIAPROGLueuAengLugIyleuMetySTPPGuaanaRghis	299
Db	957	CGGACATCTCTCATCCACCCGAGCTCAACGAGGCTCTCAATGAAGTGGAGAAITGGCAT	1016
Oy	300	GluGlyAlaI PheLyvSPheluarGrSerGluAlaValaIagInLeuTrpGlyGlnLyvLyS	319
Db	1017	GAAGGCTCTTCAAAGTCTCTCGCGCTCCAGAGCTGTGGGCCCACTRtGGGGCCAAGAAA	1076
Oy	320	LysAnSerAnMerThryTgLnLyvLeuSerArGalameArGlyTyrvTyrvLyvArg	339
Db	1077	AAGAACGACAACTGACCTACGAGAACTGAGCCGGCGCATGAGGTACTCTCAACACGG	1136
Oy	340	GluIleLeuLnuRgYalaAspGlyArgrArgLeuValTyrvLyvSPhEGlyvLyvAnSerSer	359
Db	1137	GAGATCTCTGAACGGGTGGATGGCGGCACTCGTCACAAATTGGCAAAACCTCAAGC	1196
Oy	360	GlyTrpLyvGlnGluGluValaGlyInuSerArGaen	371
Db	1197	GGCTGGAAGAGGAAGAGGTTCTCCAGAGTGGGAAC	1232

RESULT 5
US-10-025-380-1105
Sequence 1105, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongrong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skelky, Yaetr A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.

```

; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-025-380-1105

Alignment Scores:
Pred. No.: 2,42e-172 Length: 1917
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: Gaps: 2

US-08-978-217-16 (1-371) x US-10-025-380-1105 (1-1917)

Qy 1 MetAlaAlaThrcYsgJuiLseRAsnValPheSerAntYrPheAsnAlaMetYrSer 20
Db 122 ATGGCTCAACCTGTGAGATTAGCAACATTTTGTAGCAACTACTTCAGTGCATGTACAGC 181

Qy 21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db 182 TCGAGAGACTCCACCTGGCTCTGTTCCCTCTGCTCCACCTTGGGCGCGAGACTTG 241

Qy 40 ValLeuThrLeuAsnAngInGlnMetThreGluGlyProGluLysAlaSerTrpThr 59
Db 242 GTACTGACCTGTAGCAACCCCAAGATGCTATTGAGGGTACAGAGAAAGCCAGCTGGTG 301

Qy 60 SerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpLysSerTrpGlnVal 79
Db 302 GGGGAACAGCCCGGCTCTGGTTCGAGCGGAGTTCTGACCTGATCAGCTACCAAGTG 361

Qy 80 GluLysAsnLysTrpAlaLysSerSerLLeaPheSerArgCyAsnMetAspGlyVal 99
Db 362 GAGAAAGCAAGTACGACGCAAGCGCATGACTTCTCACATGTGACATGATGGCGCC 421

Qy 100 ThrLeuLysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119
Db 422 ACCCTGTGCAATTGTGCTTGTGAGAGCTGCTGTGTGCTTGTGGCCCTGGGGAGCCAA 481

Qy 120 LeuHisAlaGlnLeuAArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIle 139
Db 482 CTCATGCCCAAGCTGCGAGACCTCACTTCCAGCTCTTGATGAGCTCAGTTGATCATTT 541

Qy 140 GluLeuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGlyProPhe 159
Db 542 GAGCTGCTGAGAAAGATGGATGGCTTCCAGAGAGGCCCTA---GACCCAGGGCCCTTT 598

Qy 160 AspGlnGlySerProPheAlaGlnGluLeuLysAspGlyArgGlnAlaSerProTrp 179
Db 599 GACCAAGGCGAGCCCTTGTCCAGAGAGCTGTGACGACGCTCAGAGCCAGAGCCCTTAC 658

Qy 180 TyrCysSerThrTrpGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
Db 659 CACCCCGGACGCTGTGGCGAGAGCCCTTCCCTGACACTTGTGAGCTTCCACCGCA 718

Qy 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyLysAspValAspLeu 219
Db 719 GGAAGCTGCTGCTTCGAGAGCTCCACACTCCAGACTCCGGTGAAGGAGAGTGAAGCTG 778

Qy 220 AspleuThrGluSerLysValPheProArgAspAspPheTrpAspTrpLysLysGlu 239
Db 779 GATTCCTCAATGAGCAAGCTTCTCCAGCAGCATGATTTTCGTGACTGCACAAAGGGGAT 838

Qy 240 ProLysIleGlyLysArgLysArgGlyArgProArgLysLysSerLysGluTrpAsp 259

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Db 839 CCAGAGCGGGAAGGAGGAGAGAGCGGCGCCGAGAGCTTGACCAAGATGAGTGGAGC 898
Qy 260 CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIle 279
Db 899 TGCTCGAGGGCAAGAGAGCAAGACAGCCGCCAGAGGAGCCACCTGTGGAGTTATC 958
Qy 280 ArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHis 299
Db 959 CGGAGACATCTCATCCACCGGAGACTCAACGAGGCGCTCTGATGAGTGGAGAAATCCGCAT 1018
Qy 300 GluGlyValPheLysPheLysArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLys 319
Db 1019 GAAGGCTCTTCAAGTCTCGCGCTCCGAGCTGTGGCCCAACTATGGGCGCAAAAGAAA 1078
Qy 320 LysAsnSerAsnMetThrTrpGluLysLeuSerArgAlaMetArgTrpTrpLysArg 339
Db 1079 AAGAACAGCAACATGACTTCCAGAGAGCTTACGCGGCCACTGAGTACTACTACAAACGG 1138
Qy 340 GluIleLeuGluArgValAspGlyArgArgLeuValTrpLysPheGlyLysAsnSerSer 359
Db 1139 GAGATCCTGGAACGGGTGGATGGCGGCGAGCTGCTACAAAGTTGGCAAAACTCAAGC 1198
Qy 360 GlyTrpLysGluGluGluValGlyLysSerArgAsn 371
Db 1199 GGCTGGAAGAGAGAGAGGTTCTTCAGATCGGAAAC 1234

RESULT 6
US-09-922-217-1105
; Sequence 1105, Application US/09922217
; Patent No. US200207641A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongrong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-217-1105

Alignment Scores:
Pred. No.: 2,42e-172 Length: 1917
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: Gaps: 2

US-08-978-217-16 (1-371) x US-09-922-217-1105 (1-1917)

Qy 1 MetAlaAlaThrcYsgJuiLseRAsnValPheSerAntYrPheAsnAlaMetYrSer 20
Db 122 ATGGCTCAACCTGTGAGATTAGCAACATTTTGTAGCAACTACTTCAGTGCATGTACAGC 181

Qy 21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39

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Db 182 TGGGAGACTCCACCTGGCCTCTGTTCCCTGCTGCCACCTTTGGGGCCATGACTTG 241
Qy 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluValAspSerThr 59
Db 242 GAACTGACCTGAGCAACCCCGAGATGATGAGGATACAGAAAGCCGAGCTGTTG 301
Qy 60 SerGluArgProGlnPheThrPheSerIleThrGlnValLeuGluTrpIleSerThrGlnVal 79
Db 302 GGGGAACACCCCGAGTCTGCTGGAAGAGCGAGTCTGAGCTGATGCTGACCAAGTG 361
Qy 80 GluValAsnIleThrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99
Db 362 GAGAAAGAACAACTACACACCAAGCCGACTTGACTTCTACGATGACATGATGAGCCGC 421
Qy 100 ThrLeuCysSerCysAlaLeuGlnGluLeuValArgLeuValPheGlyProLeuGlyAspGln 119
Db 422 ACCCTCTGCAATTGTCCTTGAGGAGCTGCGTCTGCTCTTGAGGCTCTGGGGGACCA 481
Qy 120 LeuHisAlaGlnLeuValArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle 139
Db 482 CTCACATGCCACCTGAGACCTCCTCAGCTCTTGATGAGCTCAGTTGATGATCAT 541
Qy 140 GluLeuLeuGluValAspGlyMetSerPheGlnGlnSerLeuGlyAspLeuGlyProPhe 159
Db 542 GAGCTGCTGAGAAAGATGATGATGCTTCCAGAGAGCCCTA--GACCCAGGGCCCTTT 598
Qy 160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProThr 179
Db 599 GACCAAGGAGCCCTTTGCTCCAGAGAGCTGAGAGAGAGCTGAGCAAGCCGCTTAC 658
Qy 180 TyrCysSerThrThrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
Db 659 CACCCCGAGCTGTGGCCAGAGAGCCCTCCCTCGAGCTGACCTTCCACCGCA 718
Qy 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlySerAspValAspLeu 219
Db 719 GGGATGCTGCTCTCGAGCTCCACCTCTCAAGCTCCGGTGAAGATGATGAGACTTG 778
Qy 220 AspLeuThrGlnSerIleValPheProArgAspAspPheThrAspTrpIleSerGlyGln 239
Db 779 GATCCCATGATGGAGAGCTTCTCCAGAGATGTTTGGTGAATGCAAGAGGGGAT 838
Qy 240 ProLysHisGlyValArgIleValArgIleValProArgLysLeuSerIleGlyTrpAsp 259
Db 839 CCAAGACAGGGAGAGGAGAGAGAGCCCGCCGAAACCTAGCAAGAGTACTGGGAC 898
Qy 260 CysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisIleuTrpGluPheIle 279
Db 899 TGCTCGAGGGCAAGAGAGCAAGCAGCGCCAGAGGCAACCTGTTGGAGTTTCATC 958
Qy 280 ArgAspIleLeuIleHisProGluLeuAsnGlnGlyLeuMetLysTrpGluAsnArgHis 299
Db 959 CGGAGCATCTCTATCACCAGAGCTCAACGAGGCTCATTAAGTGGAGAAATCGGCT 1018
Qy 300 GluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLys 319
Db 1019 GAAGGCGCTTCAAGTCTCGGCTCCGAGGCTGTGGCCCACTATGAGGGCCAAAAA 1078
Qy 320 LysAsnSerAsnMetThrThrGlyLysLeuSerArgAlaMetArgTrpTrpLysArg 339
Db 1079 AAGAACAGAACATACCACTACAGAAAGCTGAGCCGGGCATAGGACTACTACAAACGG 1138
Qy 340 GluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer 359
Db 1139 GAGATCTCTGGAACGGGTGATGGCCGGCACTCGTCTACAAATTTGGCAAAATCTAAC 1198
Qy 360 GlyTrpLysGlnGluGluValGlyLysSerArgAsn 371
Db 1199 GGCTGGAAGAGAGAGGTTCTCCAGAGTCCGAAC 1234

RESULT 7

US-09-925-301-207
; Sequence 207, Application US/09925301

; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 207
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-207

Alignment Scores:

Pred. No.:	2,57e-172	Length:	1996
Score:	1712.00	Matches:	323
Percent Similarity:	92.74%	Conservative:	22
Best Local Similarity:	86.83%	Mismatches:	25
Query Match:	86.25%	Indels:	2
DB:	10	Gaps:	2

US-08-978-217-16 (1-371) x US-09-925-301-207 (1-1996)

Qy 1 MetaAlaThrCysGluIleSerAsnValPheSerAsnTrpPheAsnAlaMetThrSer 20
Db 141 ATGGCTGGAACCTGTGAATTAAGCAACATTTTATGAACTCTTCAAGTCAGTGCATGACAGC 200
Qy 21 SerGluAspProThrLeuAlaProAlaProPro--ThrThrPheGlyThrGluAspLeu 39
Db 201 TCGGAGAGCTCACCTTGCTGCTCTTCCCTGCTGCTGACCTTTGGGGCCGATACCTTG 260
Qy 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGlnGlyProGluValAspSerThr 59
Db 261 GAACTGACCTGAGCAACCCCGAGATGATGAGGATGAGAGAGAGAGAGAGAGAGAGAG 320
Qy 60 SerGluArgProGlnPheThrPheSerIleThrGlnValLeuGluTrpIleSerThrGlnVal 79
Db 321 GGGGAACAGCCCACTTGTGTGGAAGAGCAGAGTTCTGAGCTGATGACTACCAAGTG 380
Qy 80 GluValAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99
Db 381 GAGAGAACAACTACAG 440
Qy 100 ThrLeuCysSerCysAlaLeuGlnGluLeuValArgLeuValPheGlyProLeuGlyAspGln 119
Db 441 ACCCTCTGCAATTGTCCTTGAGAGAGCTGAGTGTGCTTGGGCTCTGGGGGACCA 500
Qy 120 LeuHisAlaGlnLeuValArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle 139
Db 501 CTCACATGCCACCTGCGAGCTTCACTTCCAGCTCTTGTGATGAGCTCAGTTGGATTCATT 560
Qy 140 GluLeuLeuGluValAspGlyMetSerPheGlnGlnSerLeuGlyAspLeuGlyProPhe 159
Db 561 GAGCTGCTGAGAAAGATGAG 617
Qy 160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProThr 179
Db 618 GACCAAGGAG 677
Qy 180 TyrCysSerThrThrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
Db 678 CACCCCGAGAGCTGTGGCGAG 737
Qy 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyLysSerAspValAspLeu 219
Db 738 GGGAGTGTGCTCTCGAGAGCTCCACTCTCAGACTCGGAGAGAGAGAGAGAGAGAGAGAG 797

QY 220 AspLeuThrgluserLysValPheProArgAspSerThrAspTyrLysGlyGlu 239
 DB 798 GATCCCTGATGCGCAAGCTCTTCCAGCGAGTGTTCGTGACTCCAGAGGGGAT 857
 QY 240 ProLysHisGlyLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAsp 259
 DB 858 CCAGACGACGGAGAAAGCGAAACGAGCGCGCCGAAAGCTGACCAAGATCTGGGAC 917
 QY 260 CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIle 279
 DB 918 TGTCTCGAGGGCAAGAGAGAGACGACCGCCAGAGACCCACTCTGGGATTCATC 977
 QY 280 ArgAspLeuLeuLeuHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHis 299
 DB 978 CGGACATCTCTCACTCCACCGGAGCTCAACGAGCGCTCAATGAGTGGAGATCGGCAT 1037
 QY 300 GluGlyValPheLysPheLeuArgSerGluAlaValAlaGluLeuTrpGluLysLys 319
 DB 1038 GAAGGCTCTTCAAGTCTCGGCTCCGAGGCTGTGCGCCCAATGAGGCGCAAGAA 1097
 QY 320 LysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrLysArg 339
 DB 1098 AAGACACGCAACATGACTTACGAGAGACTGACCGCGCCATGAGTACTACTACAAACGG 1157
 QY 340 GluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer 359
 DB 1158 GAGATCTCTGACGCGGTGATGCGCGGAGCTCTTACAAAGTTTGCAAAACTCAAGC 1217
 QY 360 GlyTrpLysGluGluGluValGlyGluSerArgAsn 371
 DB 1218 GGCTGGAAGAGAGAGAGGTTCACAGATCGGAAC 1253

RESULT 8

US-10-025-380-853/c
 ; Sequence 853, Application US/10025380
 ; Publication No. US20020182191A1

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Lodes, Michael J.
 APPLICANT: Secrist, Heather
 APPLICANT: Benson, Darin R.
 APPLICANT: Meagher, Madeline Joy
 APPLICANT: Stolk, John A.
 APPLICANT: Wang, Tongtong
 APPLICANT: Jiang, Yugu
 APPLICANT: Smith, Carole L.
 APPLICANT: King, Gordon E.
 APPLICANT: Wang, Aijun
 APPLICANT: Clapper, Jonathan D.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Vedvick Thomas S.
 APPLICANT: Carter, Darrick
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 FILE REFERENCE: 210121.471C14
 CURRENT APPLICATION NUMBER: US/10/025,380
 CURRENT FILING DATE: 2001-12-19
 NUMBER OF SEQ ID NOS: 1129
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 853
 LENGTH: 626
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-025-380-853

Alignment Scores:

Pred. No.: 8,66e-90 Length: 626
 Score: 928.50 Matches: 174
 Percent Similarity: 90.91% Conservative: 16
 Best Local Similarity: 83.25% Mismatches: 18
 Query Match: 46.78% Indels: 1
 DB: 9 Gaps: 1

US-08-978-217-16 (1-371) x US-10-025-380-853 (1-626)

QY 52 GlyProGluLysAlaSerTrpThrSerGluArgProGluInPheTrpSerLysThrGluVal 71
 DB 624 GGTACAGAGAAAGCCAGCTGTTGGGGAAACAGCCCAAGTTCGTGTAAGACCGAGTT 565
 QY 72 LeuGluTrpLysSerTyrGluValGluLysAsnLysTyrAspAlaSerSerIleAspPhe 91
 DB 564 CTGAGCTGATCAAGTCTCCAAAGTGAAGAAACAAAGTACAGACCGAAGCGCATGACTTC 505
 QY 92 SerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeu 111
 DB 504 TCACGATGTACATGTGATGCGCACCCCTCTGCAATGTGCTTGGAGAGCTGCGCTG 445
 QY 112 ValPheGlyProLeuGlyAspGluLeuHisAlaGluLeuArgAspLeuTrpSerAsnSer 131
 DB 444 GTCTTGGGCTCTTGGGGGACCAACTTCATGCCAGCTGCGAAGCTCACTTCCAGCTCT 385
 QY 132 SerAspGluLeuSerTrpIleIleGluLeuGluLysAspGlyMetSerPheGluGlu 151
 DB 384 TCTGATAGCTCAAGTTCATTTGATGAGCTCTGAGAGAGATGGCATGGCTTCCAGAG 325
 QY 152 SerLeuGlyAspLeuGlyProPheAspGlyGlySerProPheAlaGluGluLeuAsp 171
 DB 324 GCCCTA---GACCCAGGGCCCTTTGACCAAGGAGGCCCTTTGCCAGGAGCTGTGGAC 268
 QY 172 AspGlyArgGluLysSerProTyrTyrCysSerThrTyrGlyProGlyValProSerPro 191
 DB 267 GACGATGAGACGACGACCCCTTACACCCGCGAGCTGTGGCGAGAGCCCTTCCCTCC 208
 QY 192 GlySerSerAspValSerThrAlaArgThrAlaThrProGluSerSerHisAlaSerAsp 211
 DB 207 GCGAGCTCTGACGCTCTCAACCGCAGGAGCTGTGCTTCTCGAGCTCCACTCTCCAGAC 148
 QY 212 SerGlyGlySerAspValAspLeuAspLeuThrGluSerLysValPheProArgAspAsp 231
 DB 147 TCCGTTGGAAGTACGCTGACCTGAGTCCCATGATGCAAGCTCTTCCAGAGAGGT 88
 QY 232 PheThrAspTyrLysLysGlyGluProLysHisGlyLysArgLysArgGlyArgProArg 251
 DB 87 TTTCGTACTGCAAGAGGGGGATCCCAAGCAGGAGCGAAACGAGCGCGGCCGA 28
 QY 252 LysLeuSerLysGluTyrTrpAspCys 260
 DB 27 AAGCTGACAAAGATGACTGGACTGT 1

RESULT 9

US-09-922-217-853/c
 ; Sequence 853, Application US/09922217
 ; Patent No. US2002007641A1

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Lodes, Michael J.
 APPLICANT: Secrist, Heather
 APPLICANT: Benson, Darin R.
 APPLICANT: Meagher, Madeline Joy
 APPLICANT: Stolk, John A.
 APPLICANT: Wang, Tongtong
 APPLICANT: Jiang, Yugu
 APPLICANT: Smith, Carole Lynn
 APPLICANT: King, Gordon E.
 APPLICANT: Wang, Aijun
 APPLICANT: Clapper, Jonathan D.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 FILE REFERENCE: 210121.471C13
 CURRENT APPLICATION NUMBER: US/09/922,217
 CURRENT FILING DATE: 2001-08-03
 NUMBER OF SEQ ID NOS: 1124
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 853
 LENGTH: 626

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-217-853

Alignment Scores:
Pred. No.: 8,66e-90      Length: 626
Score: 928.50           Matches: 174
Percent Similarity: 90.91% Conservative: 16
Best Local Similarity: 83.25% Mismatches: 18
Query Match: 46.78%      Indels: 1
                        Gaps: 1

US-08-978-217-16 (1-371) x US-09-922-217-853 (1-626)

Oy 52 GTPGGLULYALASerTTPThSerGluAArgProGlnPheTTPSerLyThrGlnVal 71
Db 624 GGTACAGAGAGAGCCAGCTGGTTGGGGAGAACAGCCCCAGTTCTGTCCAGAACGCAAGTT 565
Oy 72 LeuGluTPPLeSerTyrGlnValGluYsaAnLyTyraSPAlaSerSerIleasphe 91
Db 564 CTGAGCTGGATCAGCTACCAAGTGAGAGAACAGTACGACGACGACGCAATTCCTTC 505
Oy 92 SerArgCysaenMetaspGlyAlaThrLeuCyserCysAlaLeuGluGluLeuArgLeu 111
Db 504 TCACATGTGACATGATGGCCGACCCCTCTCCAAATGTGCTTGAAGAGCTGGCTGTG 445
Oy 112 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSeranser 131
Db 444 GTCTTTGGGCTCTGGGGAGCCAACTCCATGCCAGCTGCGAGACCTTCCTCCAGCTCT 385
Oy 132 SeraspGluLeuSerTTPLeIleGluLeuLeuGluYsaSPGlyMetSerPheGlnGlu 151
Db 384 TCTGATGAGCTCAGTTGATGATTCGTGCTGAGAGAGATGGCATGGCTTCCAGAG 325
Oy 152 SerLeuGlyAspLeuGlyProPheaspGlnGlySerProPheAlaGlnGluLeuLeu 171
Db 324 GCCCTA---GACCCAGGGGCCCTTTGACAGGGGAGGCCCTTTGGCCAGAGAGCTGTGAC 268
Oy 172 AspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyValaProSerPro 191
Db 267 GACGGTCAAGAGAGCCAGCCCTTACCAACCCCGGAGCTGTGGGCGAGAGCCCCCTCCCC 208
Oy 192 GlySerSeraspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerasp 211
Db 207 GGCAGCTCTGACGTCTCCACCGCAGGAGCTGGTGTCCGAGGCTCCACCTCCACAGC 148
Oy 212 SerGlyGlySeraspValaSPLeuaspLeuThrGluSerLyValaPheProArgaspasp 231
Db 147 TCCGGTGAAGTGAAGTGAAGTCCGATCCACTGATGGCAGACCTTCCCGACGATGT 88
Oy 232 PheThrAspTyrLyValGlyGluProLySHisGlyLyValaGlyValaArgProArg 251
Db 87 TTTCTGACTGCAAGAGAGGGGATCCCAAGCACGGGAGAGCGAAGAGCGGCCGCCGA 28
Oy 252 LyLeuSerLyGluTyrTTPaspCys 260
Db 27 AAGCTGAGCAAGAGTACTGGGACTGT 1

RESULT 10
US-09-833-263-853/c
; Sequence 853, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolck, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833.263
; NUMBER OF SEQ ID NOS: 1093
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-833-263-853

Alignment Scores:
Pred. No.: 8,66e-90      Length: 626
Score: 928.50           Matches: 174
Percent Similarity: 90.91% Conservative: 16
Best Local Similarity: 83.25% Mismatches: 18
Query Match: 46.78%      Indels: 1
                        Gaps: 1

US-08-978-217-16 (1-371) x US-09-833-263-853 (1-626)

Oy 52 GTPGGLULYALASerTTPThSerGluAArgProGlnPheTTPSerLyThrGlnVal 71
Db 624 GGTACAGAGAGAGCCAGCTGGTTGGGGAGAACAGCCCCAGTTCTGTCCAGAACGCAAGTT 565
Oy 72 LeuGluTPPLeSerTyrGlnValGluYsaAnLyTyraSPAlaSerSerIleasphe 91
Db 564 CTGAGCTGGATCAGCTACCAAGTGAGAGAACAGTACGACGACGACGCAATTCCTTC 505
Oy 92 SerArgCysaenMetaspGlyAlaThrLeuCyserCysAlaLeuGluGluLeuArgLeu 111
Db 504 TCACATGTGACATGATGGCCGACCCCTCTCCAAATGTGCTTGAAGAGCTGGCTGTG 445
Oy 112 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSeranser 131
Db 444 GTCTTTGGGCTCTGGGGAGCCAACTCCATGCCAGCTGCGAGACCTTCCTCCAGCTCT 385
Oy 132 SeraspGluLeuSerTTPLeIleGluLeuLeuGluYsaSPGlyMetSerPheGlnGlu 151
Db 384 TCTGATGAGCTCAGTTGATGATTCGTGCTGAGAGAGATGGCATGGCTTCCAGAG 325
Oy 152 SerLeuGlyAspLeuGlyProPheaspGlnGlySerProPheAlaGlnGluLeuLeu 171
Db 324 GCCCTA---GACCCAGGGGCCCTTTGACAGGGGAGGCCCTTTGGCCAGAGAGCTGTGAC 268
Oy 172 AspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyValaProSerPro 191
Db 267 GACGGTCAAGAGAGCCAGCCCTTACCAACCCCGGAGCTGTGGGCGAGAGCCCCCTCCCC 208
Oy 192 GlySerSeraspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerasp 211
Db 207 GGCAGCTCTGACGTCTCCACCGCAGGAGCTGGTGTCCGAGCTCCACCTCCACAGC 148
Oy 212 SerGlyGlySeraspValaSPLeuaspLeuThrGluSerLyValaPheProArgaspasp 231
Db 147 TCCGGTGAAGTGAAGTGAAGTCCGATCCACTGATGGCAGACCTTCCCGACGATGT 88
Oy 232 PheThrAspTyrLyValGlyGluProLySHisGlyLyValaGlyValaArgProArg 251
Db 87 TTTCTGACTGCAAGAGAGGGGATCCCAAGCACGGGAGAGCGAAGAGCGGCCGCCGA 28
Oy 252 LyLeuSerLyGluTyrTTPaspCys 260
Db 27 AAGCTGAGCAAGAGTACTGGGACTGT 1

RESULT 11
US-10-025-380-944/c
; Sequence 944, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolck, John A.
; APPLICANT: Wang, Tonglong
```



```

? APPLICANT: Jiang, Yugu
? APPLICANT: Smith, Carole L.
? APPLICANT: King, Gordon E.
? APPLICANT: Wang, Aijun
? APPLICANT: Clapper, Jonathan D.
? APPLICANT: Skeiky, Yasir A. W.
? APPLICANT: Fanger, Gary R.
? APPLICANT: Vedvick Thomas S.
? APPLICANT: Carter, Darick
? TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
? FILE REFERENCE: 201021.471C4
? CURRENT APPLICATION NUMBER: US/10/025,380
? NUMBER OF SEQ ID NOS: 1129
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 944
? LENGTH: 563
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-025-380-944

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Db	85	CGTACGTGCAAGAAAGGGGGGATGCCAAGCAAGGAGACGGAAACGAGGCGGCCCGCAAG	26
Qy	253	LeuSerlysglturyTTPaPcy 260	
Db	25	CTGAGCAAAAGACTGTGGGACTGT 2	
RESULT 13			
US-09-833-263-944/C			
/ Sequence 944, Application US/09833263			
/ Patent No. US20020110547A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Wang, Aijun			
/ APPLICANT: Clapper, Jonathan D.			
/ APPLICANT: Stolk, John A.			
/ APPLICANT: Meagher, Madeleine J.			
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND			
/ TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE			
/ FILE REFERENCE: 210121.471C12			
/ CURRENT APPLICATION NUMBER: US/09/833,263			
/ CURRENT FILING DATE: 2001-04-10			
/ NUMBER OF SEQ ID NOS: 1093			
/ SOFTWARE: FastSeq for Windows Version 3.0			
/ SEQ ID NO 944			
/ LENGTH: 563			
/ TYPE: DNA			
/ ORGANISM: Homo sapien			
US-09-833-263-944			
Alignment Scores:			
Pred. No.:	9,24e-80	Length:	563
Score:	833.50	Matches:	157
Percent Similarity:	91.49%	Conservative:	15
Best Local Similarity:	83.51%	Mismatches:	15
Query Match:	41.99%	Indels:	1
DB:	10	Gaps:	1
US-08-978-217-16 (1-371) x US-09-833-263-944 (1-563)			
Qy	73	GLUTPILeserTYrgInValIgULysAmLyTyRAsPaLaserseTLeaSPheSer 92	
Db	562	GACTGGATCAGCTACCAAGTGGAGAAAGAACAGTACAGACGAAAGCCGATTCCTCA 503	
Qy	93	ArgCySaenMeLarPGLyLaTnTLeuCySeSeCyAlLeuGLuGLuLeuArgLeuVal 112	
Db	502	CGATGTGACAGAGTGGCGCCACCTCTGCAATGTGCTTGAGAGAGCTGGCTGTGC 443	
Qy	113	PheGLyProLeuGLyAaSPgInLeuHLeAlGLIleuArgAspLeuThSerAsnSer 132	
Db	442	TTTGGGCTCTGGGGGAGACCACTTCATGCCACCTGGAGACTCACTTCAGCTCTT 383	
Qy	133	AspGLuLeuSerTPIleIeGLuLeuGLuLyAspGLyMeSerPheGLInLuser 152	
Db	362	GATGAGCTCAATTGATCATTTGAGCTGCTGGAGAAGATGGCATGGCTTCAGAGGCC 323	
Qy	153	LeuGLyAspLeuGLyProPheAspGLInGLySerProPheAlaGLInLuleuLeuAsp 172	
Db	322	CTA--GACCCAGGGCCCTTTGACAGGGAGGCCCTTTGCCAGAGAGCTGTGAGCAC 266	
Qy	173	GLyArgGLInAlaserProTYrTYrCySeSeThTYGLyProGLyAlaProSerProGLy 192	
Db	265	GCTCAGCAAGCCACCCCTTCACACCCGCGAGCTGGGCGCAGAGACCCCTTCCCGAGC 206	
Qy	193	SeSerAspValSerThAlaArgThAlaThProGLInSerSerThAlaSerAspSer 212	
Db	205	AGCTTGAAGCTTCACCGCAGGAGACTGGTGCTTTCGAGACTCCCACTTCCAACTCC 146	
Qy	213	GLyGLySerAspValAspLeuAspLeuThrGLuSerLyValPheProArgAspAsp 232	
Db	145	GGTGAAGTGAAGTGAAGCTGGATCCCATGATGGCAAGCTTCCCGAGCATGCTTT 86	
Qy	233	ThraSPyTlyVbLyGLyGLuProLySHIGLyLyValGLyValArgGLyArgProArgLy 252	
Db	85	CGTACGTGCAAGAAAGGGGGGATGCCAAGCAAGGAGACGGAAACGAGGCGGCCCGCAAG 26	

Oy	253	LeuSerLySGuLyTyrTrpAspCyS	260
Db	25	CTGAGCAAAAGATCTGGAGCTT	2
RESULT 14			
US-10-076-622-282			
; Sequence 282, Application US/10076622			
; Publication No. US20030023036A1			
; GENERAL INFORMATION:			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Sleath, Paul R.			
; APPLICANT: Persing, David H.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER			
; FILE REFERENCE: 210121.470C11			
; CURRENT APPLICATION NUMBER: US/10/076,622			
; CURRENT FILING DATE: 2002-02-13			
; NUMBER OF SEQ ID NOS: 627			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 282			
; LENGTH: 502			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-076-622-282			
Alignment Scores:			
Pred. No.:		1,366-76	Length: 502
Score:		803.00	Matches: 149
Percent Similarity:		93.33%	Conservative: 5
Best Local Similarity:		90.30%	Mismatches: 11
Query Match:		40.45%	Indels: 0
DB:		9	Gaps: 0
US-08-978-217-16 (1-371) x US-10-076-622-282 (1-502)			
Oy	185	GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro	204
Db	6	GGCGAGAGAGCCCCCTCCCCCGGAGCTGTGACGTCTCCACCGAGGAGACTGGGCTTCT	65
Oy	205	GlnSerSerThrSalAserAspSerGlyGlySerAspValAspLeuAspLeuThrGlnSer	224
Db	66	CGAGACTCCCACTCTCAGACTCCGGTGGAAAGTGAAGTGAAGTCCGATCCACCATGATGCG	125
Oy	225	LyseValPheProArgAspAspPheThrAspTyrLysLysGlyGluProLysHisGlyLys	244
Db	126	AAGCTCTTCCCCAGCATGCTTTTCGTGATCGCAAGAAAGGGAGATCCCAAGACGGGAG	185
Oy	245	ArgLysArgGlyArgProArgLysLeuSerLysGlyGluTyrTrpAspCySLeuGluGlyLys	264
Db	186	CGGAAACGAGGCGCGGCCCGGAAAGCTGAGCAAGAAAGTACTGGGACTTCTTCGAGGGCAG	245
Oy	285	LysSerLysHisAlaProArgGlyThrHisLeuThrGluPheIleArgAspIleLeuIle	284
Db	246	AAGAGCAAGCAAGCGCCAGAGGCAACCCACTGTGGAGTTCATCCGGGACATCTTCATC	305
Oy	285	HisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGlyGlyValPheLys	304
Db	306	CACCGGAGCTCAACGAGGGCTCATGAAGTGGAGAAATGGCATGAAAGGCGTCTTCAAG	365
Oy	305	PheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsnSerAsnMet	344
Db	366	TTCTCGCGCTCCGAGGCTGTGTGCCCACTATGGGGCCAAAAAGAAACAGACACATG	425
Oy	325	ThrTyrGlyLysLeuSerAspArgAlaMetArgTyrTyrTyrTyrLysArgGluIleLeuGluArg	344
Db	426	ACCTACGAGAACTGAGAGCGGGGCGCATAGGATCTACTACAAACGGAGATCTCGGAACGG	485
Oy	345	ValAspGlyArgArg	349
Db	486	GTGATGGCCGGCCA	500
RESULT 15			

US-09-604-287A-282
; Sequence 282, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-282

Alignment Scores:
Pred. No.: 1,366-76 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
DB: 10 Gaps: 0

US-08-978-217-16 (1-371) x US-09-604-287A-282 (1-502)

QY 185 GYProGlyValAspSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
DB 6 GGGCAGAGAGCCCCCTCCCGGCACTGACCTCCACCCGAGGAGCTGGTCTTCT 65
QY 205 GlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGlnSer 224
DB 66 CGAGAGCTCCCACTCTCAGACTCCGCTGGAAGTACCTGACCTGATCCCACTGATGCG 125
QY 225 LysValPheProArgAspAspPheThrAspTyrLysLysGlyGlnProLysHisGlyLys 244
DB 126 AAGCTCTTCCCGAGAGTGTGTTCTGACTGCAAGAGGGGATCCCAAGCAGGGAAG 185
QY 245 ArgLysArgGlyLysArgProArgLysLeuSerLysGlyLysTyrTrpAspCysLeuGlnGlyLys 264
DB 186 CGGAACGAGGCGCGCCCGCAAGCTGAGCAAGAGTACTGCTGCTCGAGGGCAAG 245
QY 265 LysSerLysHisAlaProArgGlyThrHisLeuTyrGlnPheIleArgAspIleLeuIle 284
DB 246 AAGAGCAGACAGCGGCCCAAGAGCACTGAGGATTCATCCGGACATCTCATC 305
QY 285 HisProGlnLeuLysnGlnGlyLeuMetLysTrpGlnLysnArgHisGlnGlyValPheLys 304
DB 306 CACCCGAGCTCAACGAGGAGCTCATGAGTGGAGATCGCATGAAGGGGTCTTCAAG 365
QY 305 PheLeuArgSerGlnAlaValAlaGlnLeuTyrGlnLysLysLysAsnSerAsnMet 324
DB 366 TTCCTGGCTCCGAGGCTGTGGCCCAACTATGGGGCCAAAAAGAAACAGCAACATG 425
QY 325 ThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlnIleLeuGlnArg 344
DB 426 ACCTACGAGAGAGCTGAGCCGGGCGCATGAGTACTACTACAAACGGAGATCTGGAAAGG 485
QY 345 ValAspGlyArgArg 349
DB 486 GTGATGGCCGGCGA 500

Search completed: March 16, 2003, 03:36:23
Job time: 112.105 secs

